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Figure 1

1 GGAAGTCAGCAGGCGTTGGGGAGGGGTGGCGGGGGAATAGCGGCGCAGC
51 AGCCCCAGCCCTCAGAGAGACAGCAGAAAGGAGGGAGGGGTGCTGG
101 GGGACAGCCCCCACCATTCTTACCGCTATGGGCCCCAACCTCCCACTCC
151 CACCTCCCCCTCATCGGCCGGGCTAGGACACCCCCAAATCCCGTCGCCC
201 CCTTGGCACCGACACCCCCGACAGAGACAGAGACACAGCCATCCGCCACCA
251 CCGCTGCCGAGCCTGGCTGGGAGGGGCCAGCCCCCAGGCCCCCTAC
301 CCCTCTGAGGTGGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTG CTC TTC C
Met Leu Leu Leu Leu Phe Leu Leu Leu Phe L
20
10
380 TG CTG CCC ACC CTG TGG TTC TGC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys

Figure 1 (continued)

418 TAC TTC TTC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

70

80

Figure 1 (continued)

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G

90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
In Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu

100

643 GAT CTG CTT GGG ATG ATG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C

110

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly

120

130

Figure 1 (continued)

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA GGC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P

140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val

150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V

160

170

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His

180

Figure 1 (continued)

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H

190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile

200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G

210

220

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val

230

Figure 1 (continued)

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A

240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met

250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G

260

270

1130 GT GGT GAC TAT CTG AAG AAG CCT GGG GGC GGT GGG
ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCATCTTCTCCCC
1216 CACACCTACCCACCCAGTGGGCCCTGAAGCAGGGCCAAACCCCTCTTCCTT
1266 GTCTCCCCCTCTCCCCACTTATTCTCCTCTTTGGAAATCTTCAACTTCTGAA

Figure 1 (continued)

1316 GTGAATGTGGATACAGCGCCACTCCTGCCCCCTCTTGGCCCCCATCCATGG
1366 ACTCTTGCCCTCGGTGCAGTTTCCACTCTTGACCCCCACCTCCTACTGTCT
1416 TGTCTGTGGACAGTTGCCCTCCCCCTCATCTCCAGTGACTCAGCCTACAC
1466 AAGGAGGGGAACATTCCATCCCCAGTGAGTCTCTTCCATATGTGGTCTT
1516 CTCTACCCCTCTACCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGA
1566 ACAAAATCCCCCCCACCTCCAAGTCCATGGATTCAATGGACTCATCCATT
1616 TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAAGCTGATACCTGAAGCACT
1666 CCCAGGCTCATCCTGGGAGCTTTCCCTCAGCACCTTCACCTTCCCCTCCCAG
1716 TGTAGCCTCCTGTCA GTGGGGCTGGACCCCTTCTAATTCAGAGTCTCAT
1766 GCCTGCCCTTGCC CAGATGCC CAGGTCGTGCACTCTCTGGGATACCAGT
1816 TCAGTCTCCACATTCTGTGGTTTCTGTCCCCCATAGTACAGTTCTTCAGTG
1866 GACATGACCC CAGCCCTGCAGCCCTGCTGACCATCTCACCAGAC
1916 ACAAGGGGAAGAGCAGACATCAGGTGCTGCACCTCACTTCTGCCCCCTGG
1966 GGAGTTGGGGAAGGAACGAACCTGGCTGGAGGGGATAGGAGGGCTTTT

Figure 1 (continued)

2016 AATTATTCTTTTCTGTGAGGCTTCCCCCTCTCTGAGCCAGTTTCA
2066 TTTCTTCCGTGGCATTAGCCACTCCCTGCCCTCTCACTCCAGACCTGTT
2116 CCCACAAC TGGGAGGTAGGCTGGGAGCAAAAGGAGAGGGTGGACCCAG
2166 TTTTGC GTGGTGGTTTATTATTAATCTGGATAACAGCAAAAAAACTG
2216 AAAATAAAGAGAGAGAGAAAAA

Figure 2

Human LPAAT	1	MDLWPGAWM-	10	20	30	40	50
Yeast LPAAT	1	MSV-IGRFLY	YLRSVL-VVL	AL-AG----	LL-LLFLLPT	LWFCSPSAKY	F-----FKMA
E.coli LPAAT	1	M-----	-----LYIF	RL-IITVIYS	ILVCVFGSIY	-----	-----G
Maize LPAAT	1	MAI-----	---PLVLVVL	PLGLLFLLSG	LIVNAIQAVL	FVTIRPFESK	-----
Human LPAAT	51	FYNGWILFLA	VLAIPVCAVR	GRNVENMKIL	RLMLLHIKYL	-YGIRVEVRG	-----
Yeast LPAAT	51	FY-----G	VIASILCTLI	GKQHLAQWIT	ARCFYHVMKL	MLGLDV---K	-----
E.coli LPAAT	51	-----	-----CLFS	PRNPKHVATF	GHMFGRLAPL	-FGLKVECRK	-----
Maize LPAAT	51	FYRRINRFLA	EL-----	-----L	WLQLVWVVDW	WAGVKVQLHA	-----
Human LPAAT	101	AHHF-PPSQ-	-PYVVVSNHQ	SSLDLLGME	VL--PGRC--	-VPI-AKREL	-----
Yeast LPAAT	101	VUGE-ENLAK	KPYIMIANHQ	STLDIFMLGR	IF--PPGCT-	---VTAKKSL	-----
E.coli LPAAT	101	PTDA-ESYG-	-NAIYIANHQ	NNYDMVTASN	IVQ-PP----	TVTV-GKKSL	-----
Maize LPAAT	101	DEETYRSMGK	EHALIISNHR	SDIDWL-IGW	ILAQRSGCLG	STLAVMKKSS	-----
Human LPAAT	151	LWAGSAGLAC	W---LAGVIF	IDRKRTGDAI	SVMSEVAQTL	LTQDVRVWV-	-----
Yeast LPAAT	151	KYVPFLG---	WFMA LSGTYF	LDRSKRQEI	DTLNKGLENV	KKNKRALWV-	-----
E.coli LPAAT	151	LWIPFFGQLY	W---LTGNLL	IDRNNRTKAH	GTIAEVVNHF	KKRRISIMW-	-----
Maize LPAAT	151	KFLPVI GWSM	WF---AEYLF	LEERS-WAKDE	KTLKWGLQRL	KDFPRPFWLA	-----
Human LPAAT	201	-FPEGTRNHN	GS-----	-----	MLPFKRGAFH	LAVQAQVPV	-----
Yeast LPAAT	201	-FPEGTRSYT	SEL-----	-----T	MLPFKKGAFF	LAQQGKIPIV	-----
E.coli LPAAT	201	-FPEGTRSRG	RGL-----	-----	-LPFKTGAFH	AAIAAGVPII	-----
Maize LPAAT	201	LFVEGTRFTP	AKLLAAQEYA	ASQGLPAPRN	VLIPRTKGFV	SAVSIMRDFV	-----

Figure 2 (continued)

Human LPAAT	251	PIVMSSYQDF	YCKKERRFTS	GQCQVRVLPP	VPTEGLTPDD	VPALADR---
Yeast LPAAT	251	PVVVSNTSTL	VSPKYGVFNR	GCMIVRILKP	ISTENLTCKD	IGEFAEK---
E.coli LPAAT	251	PVCVSTTSNK	I--NLNRLHN	GLVIVEMLPP	IDVSQYGKDQ	VRELAH---
Maize LPAAT	251	PAIYDTT--V	IVPKDSPQPT	MLRILKGQSS	VIHVRMKRHA	MSEMPKSD
		260	270	280	290	300
Human LPAAT	301	-----	VRHSMITV-F	REISTDGRGG	GDYLLKKPGGG	G*.....
Yeast LPAAT	301	-----	VRDQMVDL-L	KEIGYSPAIN	DTTLPQ---	-----
E.coli LPAAT	301	-----	CRSIMEQK-I	AELDKVAE-	----REAAKG	V*.....
Maize LPAAT	301	VSKWCKDIFV	AKDALLDKHL	ATGTFDEEIR	PIGRPVKSLL	VTLFWSCLLL
		310	320	330	340	350
Human LPAAT	351
Yeast LPAAT	351	--AIEY---A	AL-----Q	HDKKVNKKIK	NEPVPSVSIS	NDVNTHNEGS
E.coli LPAAT	351
Maize LPAAT	351	FGAIEFFKWT	QLLSTWRGVA	FTAAGMALVT	GVMHVFIMFS	QA-----ERS
		360	370	380	390	400
Human LPAAT	401
Yeast LPAAT	401	S-----V	KKMH*
E.coli LPAAT	401
Maize LPAAT	401	SSARAARNRV	KKE*
		410	420	430	440	450

Figure 3

10	20	30	40	50	60
GGAGCGAGCT	GGCGGCGCCG	TCGGGCGCCG	GGCCGGGCCA	TGGAGCTGTG	GCCGTGTCTG
70	80	90	100	110	120
GCCGCGGCGC	TGCTGTGTCT	GCTGCTGCTG	GTGCAGCTGA	GCCGCGCGGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAGGTCTG	CCCTGTACTG	CGCGCTGTGC	TTCACGGTGT	CCGCCGTGGC	CTCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGCGG	CCGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGCG	CAGGCTGCAG
310	320	330	340	350	360
GAGGCCCGTC	CCTGTGTCAT	CGTCTCCAAC	CACCAGAGCA	TCCTGGACAT	GATGGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TTCCGGAGCG	CTGCGTGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGGC	GTCTTCTTCA	TCAACCGGCA	GCGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACCTGGGC	GAGCGCATGG	TCAGGGAGAA	CCTCAAAGTG

Figure 3 (continued)

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAACGAC	AATGGGGACC	TGCTGCCTTT	TAAGAAGGGC
610	620	630	640	650	660
GCCTTCTACC	TGGCAGTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTA	CTCTTCCTTC
670	680	690	700	710	720
TCCTCCTTCT	ACAACACCAA	GAAGAAGTTC	TTCACTTCAG	GAACAGTCAC	AGTGCAGGTG
730	740	750	760	770	780
CTGGAAGCCA	TCCCCACCAG	CGGCCTCACT	GCGGCGGACG	TCCCTGCGCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCCGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGGCA	GAGGGGACTC	CTCCCCGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCCGGGAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGCCCCCT	GGTGTCCCT	GCAGGGGGCT	CAGCTGGACC

Figure 3 (continued)

1090	1100	1110	1120	1130	1140
CTCCCCGGGC	TCGAGGGCAG	GGA CTGCGC	CCACGGCACC	TCTGGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCCGCTGGT	GGGCTGAGCC	ACAAGGCCCC	CGATGGCCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCAGACT	CACGCACCCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGGAA	TCGGGGCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGGG	GTCAGCACTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTTTT	ATAAACACAC	TCTTGGA AAA	AAAAAAAAAA	AAAAAAAAAA
1390	1400	1410	1420	1430	1440
AAA.....

Figure 4

10	20	30	40	50
GGAGCGAGCTGGCGCGCGCTCGGGCGCGCGCGGGCC	ATG	GAG	CTG	TGG
	Met	Glu	Leu	Trp
				Pro
60	70	80	90	
TGT CTG GCC GCG GCG CTG CTG TTG CTG CTG CTG	CTG	CTG	CAG	CTG
Cys Leu Ala Ala	Leu	Leu	Val	Gln
	Leu	Leu	Leu	Leu
				20
100	110	120	130	140
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC	CTG	TAC	TGC	GCG
Ser Arg Ala Ala	Glu	Phe	Tyr	Ala
	Ala	Ala	Leu	Tyr
				30
150	160	170	180	
CTG TGC TTC ACG GTG TCC GCC GTG GCC TCG CTC	GTC	TGC	CTG	CTG
Leu Cys Phe Thr	Val	Ser	Ala	Val
	Ser	Ala	Val	Cys
				Leu
				50
190	200	210	220	230
TGC CAC GGC GGC CCG ACG GTG GAG AAC ATG AGC	ATC	ATC	ATC	GGC
Cys His Gly Gly	Arg	Thr	Val	Glu
	Arg	Thr	Val	Met
				Ser
				Ile
				Gly
				Trp
				60

Figure 4 (continued)

240	250	260	270	
TTC GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC CGC TTC GAG GTG				
Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val				80
	70			
280	290	300	310	320
CGG GAC CCG CGC AGG CTG CAG GAG GCC CGT CCC TGT GTC ATC GTC				
Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val				
			90	
330	340	350	360	
TCC AAC CAC CAG AGC ATC CTG GAC ATG ATG GGC CTC ATG GAG GTC				
Ser Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val				110
	100			
370	380	390	400	410
CTT CCG GAG CGC TGC GTG CAG ATC GCC AAG CCG GAG CTC CTC TTC				
Leu Pro Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Leu Phe				
			120	
420	430	440	450	
CTG GGG CCC GTG GGC CTC ATC ATG TAC CTC GGG GGC GTC TTC TTC				
Leu Gly Pro Val Gly Leu Ile Met Tyr Leu Gly Val Phe Phe				140
	130			
460	470	480	490	500
ATC AAC CCG CAG CGC TCT AGC ACT GCC ATG ACA GTG ATG GCC GAC				
Ile Asn Arg Gln Arg Ser Ser Thr Ala Met Thr Val Met Ala Asp				
				150

Figure 4 (continued)

510	520	530	540	
CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT				
Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr				170
160				
550	560	570	580	590
CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CTG CCT TTT AAG				
Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys				
				180
600	610	620	630	
AAG GGC GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC				
Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val				200
190				
640	650	660	670	680
CCC GTG GTG TAC TCT TCC TTC TCC TCC TTC TAC AAC ACC AAG AAG				
Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys				
				210
690	700	710	720	
AAG TTC TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC				
Lys Phe Phe Thr Ser Gly Thr Val Thr Val Gln Val Leu Glu Ala				230
				220

Figure 4 (continued)

730	740	750	760	770
ATC CCC ACC AGC GGC CTC ACT GCG GCG GAC GTC CCT GCG CTC GTG				
Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val				
			240	
	790	800	810	
780				
GAC ACC TGC CAC CCG GCC ATG AGG ACC ACC TTC CTC CAC ATC TCC				
Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe Leu His Ile Ser				
				260
		250		
820	830	840	850	860
AAG ACC CCC CAG GAG AAC GGG GCC ACT GCG GGG TCT GGC GTG CAG				
Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln				
			270	
	880	890	900	910
870				920
CCG GCC CAG TAG CCCAGACCACGGCAGGGCATGACCTGGGAGGCAGGTGGAAGC				
Pro Ala Gln ***				
	950	960	970	980
930				
CGATGGCTGGAGGATGGGCAGAGGGGACTCCTCCCGGCTTCCAATAACCACTCTGTCCGG				
	1000	1010	1020	1030
				1040
1000				
CTCCCCCAGCTCTCACTCAGCCCCGGGAAGCAGGAAGCCCCCTTCTGTCACTGGTCTCAGAC				
	1050	1060	1070	1080
				1090
				1100
ACAGGCCCCCTGGTGTCCCCCTGCAGGGGGCTCAGCTGGACCCCTCCCGGGCTCGAGGGCAG				
990				

Figure 4 (continued)

1110	1120	1130	1140	1150	1160
	GGACTCGGCCACGGCACCTCTGGGNGCTGGNTGATAAAGATGAGGCTTGCGGCTGTG				
1170	1180	1190	1200	1210	1220
	GCCCGCTGGTGGCTGAGCCACAAGGCCCCCGATGGCCAGGAGCAGATGGGAGGACCCC				
1230	1240	1250	1260	1270	1280
	GAGCCAGGAGTCCAGACTCACGCACCCCTGGGCCACAGGAGCCGGGAATCGGGGCTG				
1290	1300	1310	1320	1330	1340
	CTGCTCCTGCTGGCCTGAAGAACTCTGTGGGTCAGCACTGTACTCCGTTGCTTTTTTT				
1350	1360	1370	1380		
	ATAAACACACTCTTGGAAAAAATAAAAAAATAAAAAAATAAAAAA				

Figure 5
Alignment of LPAAT Sequences.

Human LPAAT- β	1	10	20	30	40	50
Human LPAAT- α	1	-----	-----	<u>MEL</u> <u>WPC</u> ----- <u>LA</u> <u>AALLLLLLLV</u>		
Yeast LPAAT	1	-----	-----	<u>MDL</u> <u>WPGAWMLLLL</u> <u>LFL</u> <u>LLL</u> <u>FLLP</u>		
E.coli LPAAT	1	-----	-----	<u>MSV</u> -- <u>IGRFL</u> <u>YVL</u> <u>RSVL</u> <u>WLALA</u>		
H.influenzae	1	-----	-----	-----		
S.typhimurium	1	-----	-----	-----		
L.douglasi	1	<u>MAKIR</u> <u>SS</u> - <u>L</u> <u>RNR</u> -----	-----	<u>RQLKP</u> <u>AVA</u> <u>ATAD</u> -- <u>D</u> <u>DKDGV</u> <u>FMV</u> --		
C. nificera	1	<u>MDASCA</u> <u>SSFL</u> <u>RGRCL</u> <u>ESCFK</u> <u>ASFG</u> <u>MSQPKD</u> <u>AAGQ</u> <u>PSRRPA</u> <u>DADD</u> <u>FFIVDD</u>				
Human LPAAT- β	51	60	70	80	90	100
Human LPAAT- α	51	<u>QL</u> -- <u>SPA</u> <u>AE</u> <u>FYAK</u> <u>VAL</u> - <u>YC</u> <u>ALCF</u> <u>T</u> <u>VS</u> <u>AVA</u> <u>SLVCL</u> <u>L</u> <u>CHGG</u> <u>RTVEN</u> <u>M</u> - <u>SII</u>				
Yeast LPAAT	51	<u>TLWF</u> <u>CS</u> <u>ESAK</u> <u>YFF</u> <u>KMAF</u> - <u>YN</u> <u>GWIL</u> <u>FLAVLA</u> <u>IPVCAV</u> -- <u>RG</u> <u>RNVEN</u> <u>M</u> - <u>KIL</u>				
E.coli LPAAT	51	<u>G</u> -- <u>CG</u> ----- <u>FY</u> -----	-----	<u>GVIA</u> <u>SI</u> <u>LCT</u> <u>LIGKQ</u> <u>HLAQWI</u> - <u>TAR</u>		
H.influenzae	51	----- <u>ML</u> <u>YI</u> <u>FRLI</u> <u>TVI</u> <u>YS</u> <u>IL</u> <u>VC</u> -----	<u>VFG</u> <u>SI</u> <u>YCL</u> <u>FS</u> <u>PRN</u> <u>PKHV</u> ----- <u>ATF</u>			
S.typhimurium	51	----- <u>ML</u> <u>KL</u> <u>LRI</u> <u>FL</u> <u>ML</u> <u>IQ</u> <u>ILIC</u> -----	<u>VLG</u> <u>TI</u> <u>YS</u> <u>FT</u> <u>REKN</u> <u>PSNV</u> ----- <u>GIV</u>			
L.douglasi	51	----- <u>ML</u> <u>YI</u> <u>FRLI</u> <u>TVI</u> <u>YS</u> <u>IL</u> <u>VC</u> -----	<u>VFG</u> <u>SI</u> <u>YCL</u> <u>FS</u> <u>PRN</u> <u>PKHV</u> ----- <u>ATF</u>			
C. nificera	51	----- <u>LL</u> <u>SC</u> <u>FKIF</u> <u>VC</u> <u>FAFT</u> <u>WLI</u> <u>T</u> <u>AVANG</u> <u>LIM</u> <u>W</u> <u>LLP</u> <u>WP</u> <u>YMRIR</u> <u>IGNLY</u>				
	51	<u>DRW</u> <u>TVI</u> <u>LSV</u> <u>VRI</u> <u>ACFL</u> -- <u>SMW</u> <u>TVI</u> <u>VN</u> <u>MIMI</u> <u>L</u> <u>LP</u> <u>WP</u> <u>YARI</u> <u>QGNLY</u>				

Figure 5 (continued)

	110	120	130	140	150
Human LPAAT- β	101 <u>GW</u> <u>FV</u> <u>RS</u> <u>F</u> <u>KY</u> -	-- <u>FY</u> <u>GL</u> <u>RF</u> <u>EV</u>	<u>RD</u> <u>PR</u> <u>RL</u> <u>Q</u> <u>EAR</u>	<u>PC</u> <u>VI</u> <u>VS</u> <u>NH</u> <u>QS</u>	<u>I</u> <u>LD</u> <u>MM</u> <u>GL</u> <u>MEV</u>
Human LPAAT- α	101 <u>RL</u> <u>ML</u> <u>I</u> <u>HI</u> <u>KY</u> -	-- <u>LY</u> <u>G</u> <u>IR</u> <u>VEV</u>	<u>RG</u> <u>AH</u> <u>FP</u> <u>PSQ</u>	<u>PY</u> <u>VV</u> <u>VS</u> <u>NH</u> <u>QS</u>	<u>S</u> <u>LD</u> <u>IL</u> <u>GM</u> <u>MEV</u>
Yeast LPAAT	101 <u>CFY</u> - <u>HV</u> <u>M</u> <u>KL</u> -	-- <u>ML</u> <u>GL</u> <u>DKV</u>	<u>VGE</u> <u>EN</u> <u>LAK</u> - <u>K</u>	<u>PY</u> <u>IM</u> <u>IAN</u> <u>HQS</u>	<u>T</u> <u>LD</u> <u>IF</u> <u>ML</u> <u>GRI</u>
E.coli LPAAT	101 <u>GH</u> <u>MF</u> <u>GRL</u> ---	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VEC</u>	<u>RK</u> <u>P</u> <u>TD</u> <u>AE</u> <u>SYG</u>	<u>NA</u> <u>IY</u> <u>IAN</u> <u>HQN</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>ASNI</u>
H.influenzae	101 <u>AR</u> <u>WF</u> <u>GRL</u> - <u>FT</u>	<u>YPL</u> <u>F</u> <u>GL</u> <u>K</u> <u>VEH</u>	<u>RIP</u> <u>QD</u> <u>KQIS</u>	<u>RA</u> <u>IY</u> <u>IGN</u> <u>HQN</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>ISYM</u>
S.typhimurii	101 <u>GH</u> <u>MF</u> <u>GRL</u> - <u>FT</u>	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VEC</u>	<u>RK</u> <u>P</u> <u>AD</u> <u>AE</u> <u>NYG</u>	<u>NA</u> <u>IY</u> <u>IAN</u> <u>HQN</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>AANI</u>
L.douglassi	101 <u>GH</u> <u>I</u> <u>IG</u> <u>LV</u> --	<u>IT</u> <u>WY</u> <u>GI</u> <u>PIKI</u>	<u>QG</u> <u>SE</u> <u>HI</u> <u>KKRA</u>	<u>IFT</u> <u>YI</u> <u>SN</u> <u>HAS</u>	<u>PI</u> <u>DA</u> <u>FF</u> <u>V</u> <u>MW</u>
C. nucifera	101 <u>GH</u> <u>VT</u> <u>GR</u> <u>ML</u> <u>FT</u>	<u>MW</u> <u>IL</u> <u>GN</u> <u>PITI</u>	<u>EG</u> <u>SE</u> <u>FS</u> <u>NT</u> <u>RA</u>	<u>I</u> -- <u>YI</u> <u>CN</u> <u>HAS</u>	<u>LV</u> <u>D</u> <u>IF</u> <u>IL</u> <u>MW</u>
	160	170	180	190	200
Human LPAAT- β	151 <u>LP</u> <u>ER</u> <u>CV</u> <u>Q</u> <u>IAK</u>	<u>RE</u> <u>LL</u> <u>FL</u> <u>GPV</u> -	-- <u>GL</u> <u>IM</u> <u>Y</u> <u>LG</u> <u>V</u>	<u>FF</u> <u>IN</u> <u>RQ</u> <u>RS</u> <u>ST</u>	<u>AM</u> <u>T</u> -- <u>VM</u> <u>ADL</u>
Human LPAAT- α	151 <u>LP</u> <u>GR</u> <u>CV</u> <u>PIAK</u>	<u>RE</u> <u>LL</u> <u>W</u> <u>AGSA</u> -	-- <u>GL</u> <u>AC</u> <u>W</u> <u>LAGV</u>	<u>IF</u> <u>ID</u> <u>RK</u> <u>RT</u> <u>GD</u>	<u>AI</u> <u>S</u> -- <u>VM</u> <u>SEV</u>
Yeast LPAAT	151 <u>FP</u> <u>PG</u> <u>CT</u> <u>VTAK</u>	<u>KS</u> <u>LK</u> <u>W</u> <u>PFL</u> -	-- <u>GW</u> <u>F</u> <u>MA</u> <u>LSGT</u>	<u>YF</u> <u>LD</u> <u>RS</u> <u>KRQE</u>	<u>AI</u> <u>D</u> -- <u>T</u> <u>INKG</u>
E.coli LPAAT	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>TVGK</u>	<u>KS</u> <u>LL</u> <u>W</u> <u>IPFF</u> -	-- <u>GQ</u> <u>LY</u> <u>W</u> <u>LTGN</u>	<u>LL</u> <u>ID</u> <u>RN</u> <u>NR</u> <u>TK</u>	<u>AH</u> <u>G</u> -- <u>T</u> <u>IAEV</u>
H.influenzae	151 <u>VQ</u> <u>PR</u> <u>IV</u> <u>SVGK</u>	<u>KS</u> <u>LI</u> <u>W</u> <u>IPFF</u>	<u>TG</u> <u>ILY</u> <u>W</u> <u>VTGN</u>	<u>IF</u> <u>LD</u> <u>RE</u> <u>NR</u> <u>TK</u>	<u>AH</u> <u>N</u> -- <u>T</u> <u>MSQL</u>
S.typhimurii	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>TVGK</u>	<u>KS</u> <u>LL</u> <u>W</u> <u>IPFF</u>	<u>TG</u> <u>Q</u> <u>LY</u> <u>W</u> <u>LTGN</u>	<u>LL</u> <u>ID</u> <u>RN</u> <u>NR</u> <u>AK</u>	<u>AH</u> <u>S</u> -- <u>T</u> <u>IAAV</u>
L.douglassi	151 <u>AP</u> <u>IG</u> <u>TV</u> <u>GVAK</u>	<u>KE</u> <u>VI</u> <u>W</u> <u>YP</u> <u>ILG</u>	<u>Q</u> -- <u>LY</u> <u>T</u> <u>LAH</u>	<u>IR</u> <u>ID</u> <u>RS</u> <u>NPAA</u>	<u>AI</u> <u>Q</u> <u>S</u> <u>F</u> <u>IM</u> <u>KEA</u>
C. nucifera	151 <u>IP</u> <u>KG</u> <u>TV</u> <u>TJAK</u>	<u>KE</u> <u>II</u> <u>W</u> <u>Y</u> <u>PLFG</u>	<u>Q</u> <u>PT</u> <u>LY</u> <u>V</u> <u>LANH</u>	<u>QR</u> <u>ID</u> <u>RS</u> <u>NP</u> <u>SA</u>	<u>AI</u> <u>ES</u> -- <u>I</u> <u>KEV</u>

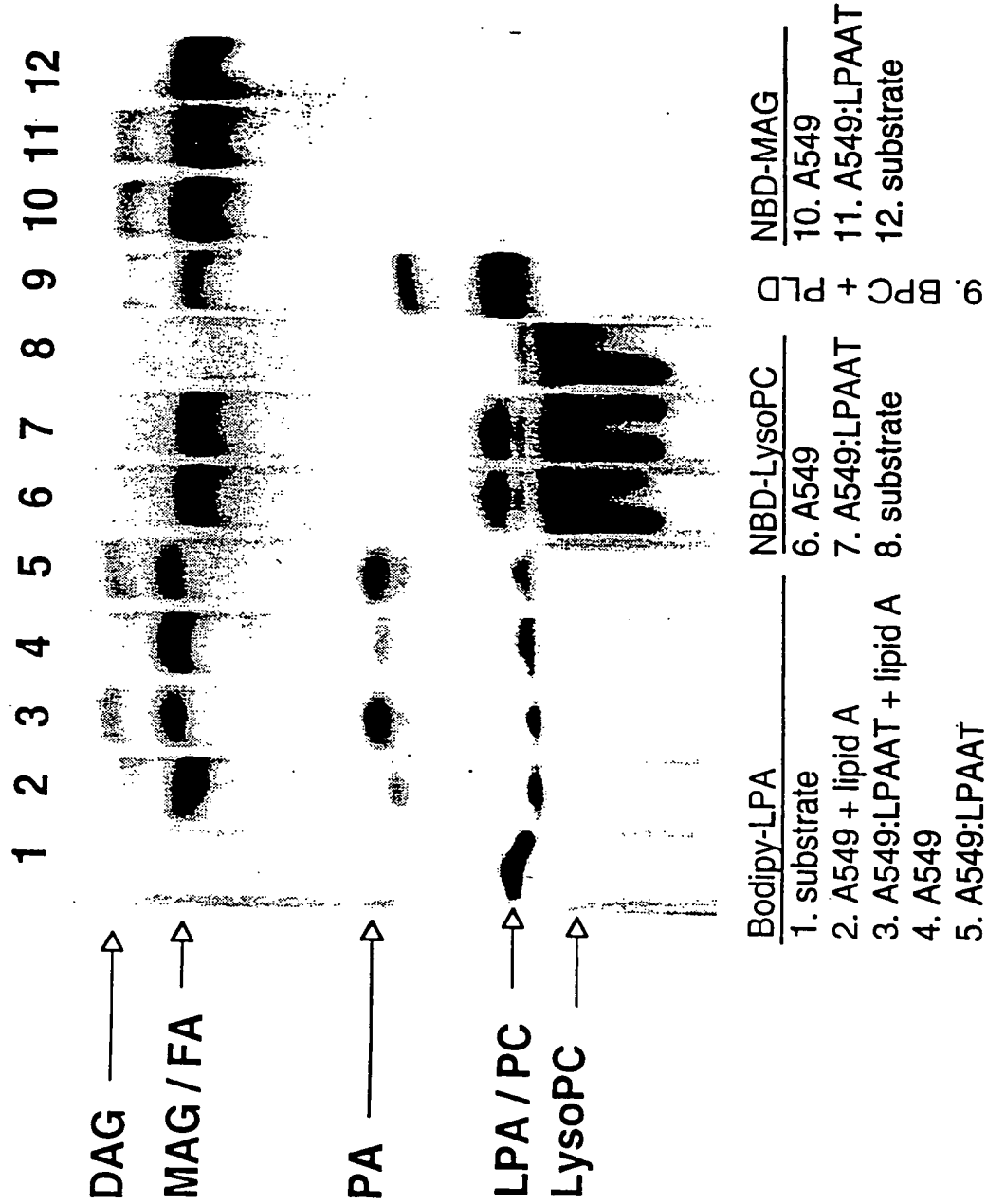
Figure 5 (continued)

Human LPAAT-β	201	<u>GERMREN</u> <u>LK</u>	<u>VW</u> <u>I</u> <u>Y</u> <u>PE</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>D</u> <u>N</u> <u>G</u> <u>D</u> <u>L</u>	<u>---</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>K</u> <u>G</u> <u>A</u> <u>F</u> <u>Y</u> <u>L</u>	<u>---</u> <u>A</u>	<u>V</u> <u>Q</u> <u>A</u> <u>Q</u> <u>V</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>V</u>	250
Human LPAAT-α	201	<u>AQ</u> <u>T</u> <u>L</u> <u>L</u> <u>T</u> <u>Q</u> <u>D</u> <u>V</u> <u>R</u>	<u>VW</u> <u>V</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>H</u> <u>N</u> <u>G</u> <u>S</u> <u>M</u>	<u>---</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>R</u> <u>G</u> <u>A</u> <u>F</u> <u>H</u> <u>L</u>	<u>---</u> <u>A</u>	<u>V</u> <u>Q</u> <u>A</u> <u>Q</u> <u>V</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>I</u>	250
Yeast LPAAT	201	<u>LEN</u> <u>V</u> <u>K</u> <u>K</u> <u>N</u> <u>K</u> <u>R</u> <u>A</u>	<u>LW</u> <u>V</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>Y</u> <u>T</u> <u>S</u> <u>E</u> <u>L</u> <u>T</u> <u>M</u> <u>L</u> <u>P</u> <u>F</u>		<u>K</u> <u>K</u> <u>G</u> <u>A</u> <u>F</u> <u>H</u> <u>L</u>	<u>---</u> <u>A</u>	<u>Q</u> <u>Q</u> <u>K</u> <u>I</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>V</u>	250
E.coli LPAAT	201	<u>VN</u> <u>H</u> <u>F</u> <u>K</u> <u>K</u> <u>R</u> <u>R</u> <u>I</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u>	<u>---</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u>	<u>---</u> <u>H</u> <u>A</u> <u>A</u>	<u>I</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>	250
H.influenzae	201	<u>ARR</u> <u>I</u> <u>N</u> <u>E</u> <u>D</u> <u>N</u> <u>L</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>N</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u>	<u>---</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> <u>T</u> <u>H</u> <u>A</u> <u>A</u>		<u>I</u> <u>S</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>	250
S.typhimurii	201	<u>VN</u> <u>H</u> <u>F</u> <u>K</u> <u>K</u> <u>R</u> <u>R</u> <u>I</u> <u>S</u>	<u>IW</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>R</u> <u>G</u> <u>R</u> <u>G</u> <u>L</u>	<u>---</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>T</u> <u>G</u> <u>A</u> <u>F</u> <u>T</u> <u>H</u> <u>A</u> <u>A</u>		<u>I</u> <u>A</u> <u>A</u> <u>G</u> <u>V</u> <u>P</u> <u>I</u> <u>I</u> <u>P</u> <u>V</u>	250
L.douglasi	201	<u>VR</u> <u>V</u> <u>I</u> <u>T</u> <u>H</u> <u>K</u> <u>N</u> <u>L</u> <u>S</u>	<u>L</u> <u>I</u> <u>M</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>C</u> <u>D</u> <u>G</u> <u>R</u> <u>L</u>	<u>---</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>K</u> <u>G</u> <u>F</u> <u>V</u> <u>H</u> <u>L</u>	<u>---</u> <u>A</u>	<u>L</u> <u>Q</u> <u>S</u> <u>H</u> <u>L</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>M</u>	250
C. nucifera	201	<u>AR</u> <u>A</u> <u>W</u> <u>K</u> <u>N</u> <u>L</u> <u>S</u>	<u>L</u> <u>I</u> <u>I</u> <u>F</u> <u>P</u> <u>E</u> <u>G</u> <u>T</u> <u>R</u> <u>S</u>	<u>K</u> <u>T</u> <u>G</u> <u>R</u> <u>L</u>	<u>---</u> <u>L</u> <u>P</u> <u>F</u>	<u>K</u> <u>K</u> <u>G</u> <u>F</u> <u>I</u> <u>H</u> <u>F</u> <u>T</u> <u>I</u> <u>A</u>		<u>L</u> <u>Q</u> <u>T</u> <u>R</u> <u>L</u> <u>P</u> <u>I</u> <u>V</u> <u>P</u> <u>M</u>	250
Human LPAAT-β	251	<u>VY</u> <u>S</u> <u>S</u> <u>F</u> <u>S</u> <u>S</u>	<u>---</u> <u>F</u>	<u>Y</u> <u>N</u> <u>T</u> <u>K</u> <u>K</u> <u>F</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>I</u> <u>V</u> <u>I</u> <u>Q</u> <u>V</u> <u>L</u> <u>E</u> <u>A</u>	<u>I</u> <u>P</u> <u>T</u> <u>S</u> <u>G</u> <u>L</u> <u>T</u> <u>A</u> <u>A</u> <u>D</u>		<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>V</u> <u>D</u> <u>I</u> <u>C</u> <u>H</u> <u>R</u>	300
Human LPAAT-α	251	<u>VM</u> <u>S</u> <u>S</u> <u>Y</u> <u>Q</u> <u>D</u>	<u>---</u> <u>F</u>	<u>Y</u> <u>C</u> <u>K</u> <u>K</u> <u>R</u> <u>R</u> <u>F</u> <u>T</u> <u>S</u>	<u>G</u> <u>Q</u> <u>Q</u> <u>V</u> <u>R</u> <u>V</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>P</u> <u>T</u> <u>E</u> <u>G</u> <u>L</u> <u>T</u> <u>P</u> <u>D</u> <u>D</u>		<u>V</u> <u>P</u> <u>A</u> <u>L</u> <u>A</u> <u>D</u> <u>R</u> <u>V</u> <u>R</u> <u>H</u>	300
Yeast LPAAT	251	<u>V</u> <u>S</u> <u>N</u> <u>I</u> <u>S</u> <u>T</u>	<u>---</u> <u>L</u>	<u>V</u> <u>S</u> <u>P</u> <u>K</u> <u>I</u> <u>G</u> <u>V</u> <u>F</u> <u>N</u> <u>R</u>	<u>G</u> <u>M</u> <u>I</u> <u>V</u> <u>R</u> <u>I</u> <u>L</u> <u>K</u> <u>P</u>	<u>I</u> <u>S</u> <u>T</u> <u>E</u> <u>N</u> <u>L</u> <u>T</u> <u>K</u> <u>D</u> <u>K</u>		<u>I</u> <u>G</u> <u>E</u> <u>F</u> <u>A</u> <u>E</u> <u>K</u> <u>V</u> <u>R</u> <u>D</u>	300
E.coli LPAAT	251	<u>CV</u> <u>S</u> <u>T</u> <u>T</u> <u>S</u>	<u>---</u>	<u>N</u> <u>K</u>	<u>I</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>I</u> <u>H</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>Q</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u> <u>C</u> <u>R</u> <u>---</u>	300
H.influenzae	251	<u>V</u> <u>C</u> <u>S</u> <u>S</u> <u>T</u> <u>H</u>	<u>---</u>	<u>N</u> <u>K</u>	<u>I</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>W</u> <u>D</u> <u>N</u>	<u>G</u> <u>K</u> <u>V</u> <u>I</u> <u>C</u> <u>E</u> <u>I</u> <u>M</u> <u>D</u> <u>P</u>	<u>I</u> <u>D</u> <u>V</u> <u>S</u> <u>G</u> <u>Y</u> <u>T</u> <u>K</u> <u>D</u> <u>N</u>	<u>V</u> <u>R</u> <u>D</u> <u>L</u> <u>A</u> <u>A</u> <u>Y</u> <u>C</u> <u>H</u> <u>F</u>	300
S.typhimurii	251	<u>CV</u> <u>S</u> <u>N</u> <u>I</u> <u>S</u>	<u>---</u>	<u>N</u> <u>K</u>	<u>V</u> <u>N</u> <u>L</u> <u>N</u> <u>R</u> <u>I</u> <u>N</u> <u>N</u>	<u>G</u> <u>L</u> <u>V</u> <u>I</u> <u>V</u> <u>E</u> <u>M</u> <u>L</u> <u>P</u> <u>P</u>	<u>V</u> <u>D</u> <u>V</u> <u>S</u> <u>E</u> <u>X</u> <u>G</u> <u>K</u> <u>D</u> <u>Q</u>	<u>V</u> <u>R</u> <u>E</u> <u>L</u> <u>A</u> <u>A</u> <u>H</u> <u>C</u> <u>R</u> <u>F</u>	300
L.douglasi	251	<u>I</u> <u>L</u> <u>T</u> <u>G</u> <u>T</u> <u>H</u> <u>L</u> <u>A</u> <u>W</u> <u>F</u>		<u>T</u> <u>R</u> <u>K</u> <u>G</u> <u>I</u> <u>F</u> <u>R</u> <u>V</u> <u>R</u> <u>P</u>	<u>V</u> <u>P</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>L</u> <u>P</u> <u>P</u>	<u>I</u> <u>N</u> <u>T</u> <u>D</u> <u>D</u> <u>W</u> <u>T</u> <u>V</u> <u>D</u> <u>K</u>		<u>I</u> <u>D</u> <u>D</u> <u>V</u> <u>V</u> <u>K</u> <u>M</u> <u>I</u> <u>H</u> <u>D</u>	300
C. nucifera	251	<u>V</u> <u>L</u> <u>T</u> <u>G</u> <u>T</u> <u>H</u> <u>L</u> <u>A</u> <u>W</u>	<u>---</u>	<u>---</u> <u>R</u> <u>K</u> <u>N</u> <u>S</u> <u>L</u> <u>R</u> <u>V</u> <u>R</u> <u>P</u>	<u>A</u> <u>P</u> <u>I</u> <u>T</u> <u>V</u> <u>K</u> <u>Y</u> <u>F</u> <u>S</u> <u>P</u>	<u>I</u> <u>K</u> <u>T</u> <u>D</u> <u>D</u> <u>W</u> <u>E</u> <u>E</u> <u>E</u> <u>K</u>		<u>I</u> <u>N</u> <u>H</u> <u>Y</u> <u>V</u> <u>E</u> <u>M</u> <u>I</u> <u>H</u> <u>F</u>	300

Figure 5 (continued)

	310	320	330	340	350
Human LPAAT- β	301 <u>AMRTTFIHIS</u>	<u>KTPQENGATA</u>	<u>GSGVQPAQ*</u>	-----	-----
Human LPAAT- α	301 <u>SMLTVFREIS</u>	<u>TDGRGGDYL</u>	<u>KKPGGG*</u>	-----	-----
Yeast LPAAT	301 <u>QMVDILKEIG</u>	<u>YSPAINDTTL</u>	<u>PPQAIEYAAL</u>	<u>QHDKKVNKKI</u>	<u>KNEIPVPSVSI</u>
E.coli LPAAT	301 <u>-SIMEQKIAE</u>	<u>LDKEVA</u>	<u>-ER EAAGKV*</u>	-----	-----
H.influenzae	301 <u>TDLMEKRIAE</u>	<u>LDEEIA</u>	-----	<u>KGN*</u>	-----
S.typhimurii	301 <u>TALMEQKIAE</u>	<u>LDKEVA</u>	<u>-ER EATCKV*</u>	-----	-----
L.douglassi	301 <u>IYVRNLPASQ</u>	<u>KPIGS</u>	<u>-TNR</u>	<u>-S-K*</u>	-----
C. nucifera	301 <u>TALYVDHLPE</u>	<u>SQKPLVSKGR</u>	<u>DASGRNS*</u>	-----	-----
	360	370	380	390	
Human LPAAT- β	351 -----
Human LPAAT- α	351 -----
Yeast LPAAT	351 <u>SNDVNTHNEG</u>	<u>SSVKKMH*</u>
E.coli LPAAT	351 -----
H.influenzae	351 -----
S.typhimurii	351 -----
L.douglassi	351 -----
C. nucifera	351 -----

Figure 6



TLC Analysis of Acyltransferase Activity

**Induction of TNF in A549 LPAAT or A549
cells stimulated with mTNF and IL-1**

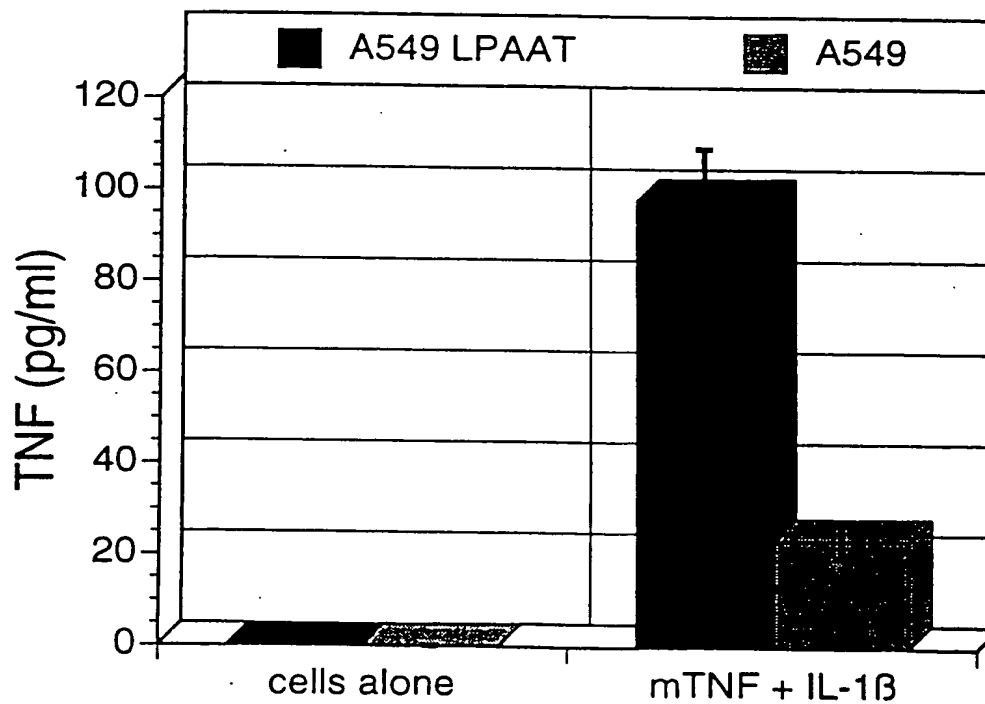


Figure 7

**Induction of IL-6 in A549 LPAAT or A549
cells stimulated with mTNF and IL-1**

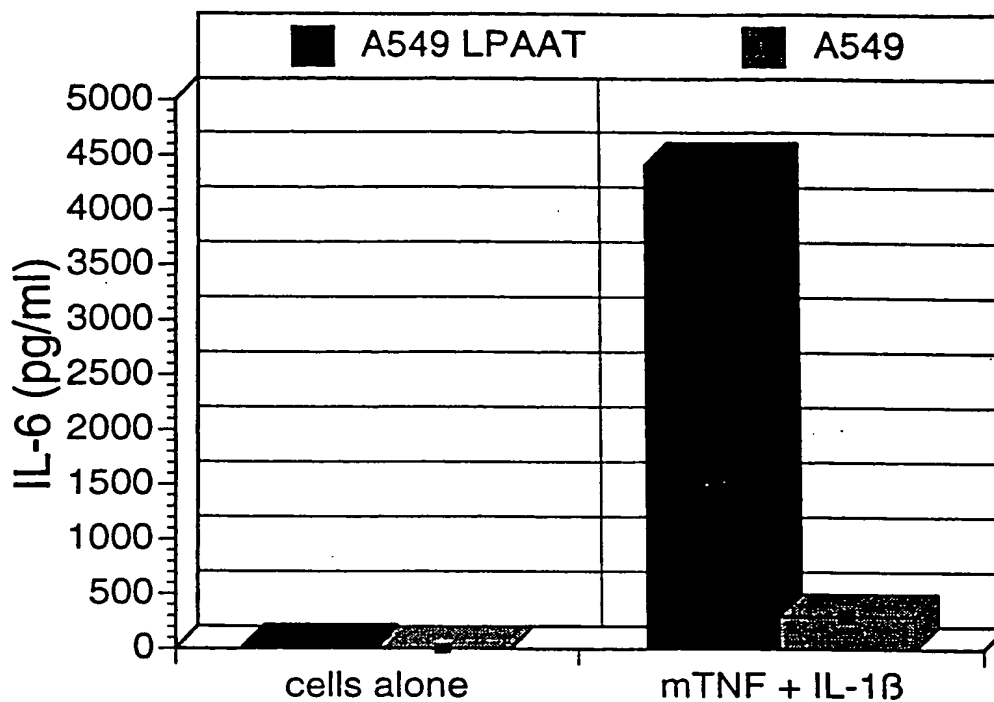


Figure 8

Title: METHOD OF SCREENING
COMPOUNDS THAT INHIBIT
LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE
Inventors: David W. LEUNG et al.
Docket No.: 077319-0383

Figure 9 Translated sequence of human LPAAT-yl

TCTATGAAACCAACATACATGGCGTTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG	60
GGCAGGTGTCTGGCTTGTCACCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGC	120
TGACCTTGTCCTTGGACGGCTGTCCTCAGCGAGGGGCGTGCACCCGCTCCTGAGCAGC	180
GCC ATG GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC	225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His	
5 10	
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC	270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn	
15 20 25	
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG	315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln	
30 35 40	
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC	360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser	
45 50 55	
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA	405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr	
60 65 70	
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC	450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His	
75 80 85	
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT	495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys	
90 95 100	
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG	540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys	
105 110 115	
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG	585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp	
120 125 130	
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG	630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu	
135 140 145	
GAG GAC CGG GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC	675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp	
150 155 160	
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC	720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg	
165 170 175	
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT	765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala	
180 185 190	
AAG GGG CTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG	810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys	
195 200 205	
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT	855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala	
210 215 220	
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC	900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC	945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys	
240 245 250	
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA	990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu	
255 260 265	
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC	1035

Inventors: David W. LEUNG et al.
Docket No.: 077319-0383

[illegible]

Title: METHOD OF SCREENING
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LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE

Inventors: David W. LEUNG et al.

Docket No.: 077319-0383

Figure 10 Translated sequence of LPAAT-γ2 cDNA

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCCTCAACTGCCGCCTCGCC	61
TACTCACTCTGGAGCCTAGCACAAAAGTAGAAGCAACCCAAGCACCTGTCACTGGAGACT	121
AATTATGCGGCACCCATACAGGGACCCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTTAAAGCGAAAAAGGAAGTATACAACAAAGTCCATAACTGGTC ATG CTG	238
	Met Leu
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

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Figure 10 (continued)

260	265	270	
CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT GTG GGA GCA GCT TCC			1093
Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser			
275	280	285	
TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT GAG ATA GAA AAA GGC			1138
Phe Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly			
290	295	300	
TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA AAG GAA TAA TTAATGGC			1185
Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu ***			
305	310		
TGTGACTGAACACACGCGGCCCTGACGGTGGTATCCAGTTAACTCAAAACCAACACACAG			1245
AGTGCAGGAAAAGACAATTAGAACTATTTTTCTTATTAAGTGGTGAATATTAACAA			1305
AACTTGAGCCAAGAGTAAAGAATTCAGAAGGCCTGTCAGGTGAAGTCTTCAGCCTCCCAC			1365
AGCGCAGGGTCCCAGCATCTCCACGCGCGCCCGTGGGAGGTGGGTCCGGCCGGAGAGGCC			1425
TCCCGCGGACGCCGTCTCTCCAGAACTCCGCTTCCAAGAGGGACCTTTGGCTGCTTTCTC			1485
TCCTTAACTTAGATCAAATTTTAAAAAAAAAAAAAAAAA			1523

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TGA	CCC	CAG	CGG	CTC	CAT	TCT	CAG	CTT	TCT	GGT	TTCT	CTA	AAG	TCC	ATG	TGCC	AAAG	GGT	TGCC	AG	61
GA	AGG	A	GAC	GC	CTT	CCT	GAG	T	CCT	G	GAT	CTT	TCT	CTT	CT	TGG	AA	TCT	TTG	ACT	121
TA	GTT	AT	TTT	AT	TTT	TCT	GA	ATA	AAG	AG	CGT	CC	ACG	CATC	ATG	GAC	CTC	GCG	GGA	CTG	175
													Met	Asp	Leu	Ala	Gly	Leu			
CTG	AAG	TCT	CAG	TTC	CTG	TGC	CAC	CTG	GTC	TTC	TGC	TAC	GTC	TTT							220
Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	Val	Phe	Cys	Tyr	Val	Phe							
			10					15					20								
ATT	GCC	TCA	GGG	CTA	ATC	ATC	AAC	ACC	ATT	CAG	CTC	TTC	ACT	CTC							265
Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	Ile	Gln	Leu	Phe	Thr	Leu							
			25					30					35								
CTC	CTC	TGG	CCC	ATT	AAC	AAG	CAG	CTC	TTC	CGG	AAG	ATC	AAC	TGC							310
Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	Phe	Arg	Lys	Ile	Asn	Cys							
			40					45					50								
AGA	CTG	TCC	TAT	TGC	ATC	TCA	AGC	CAG	CTG	GTG	ATG	CTG	CTG	GAG							355
Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu	Leu	Glu							
			55					60					65								
TGG	TGG	TCG	GGC	ACG	GAA	TGC	ACC	ATC	TTC	ACG	GAC	CCG	CGC	GCC							400
Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg	Ala							
			70					75					80								
TAC	CTC	AAG	TAT	GGG	AAG	GAA	AAT	GCC	ATC	GTG	GTT	CTC	AAC	CAC							445
Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	Ile	Val	Val	Leu	Asn	His							
			85					90					95								
AAG	TTT	GAA	ATT	GAC	TTT	CTG	TGT	GGC	TGG	AGC	CTG	TCC	GAA	CGC							490
Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	Trp	Ser	Leu	Ser	Glu	Arg							
			100					105					110								
TTT	GGG	CTG	TTA	GGG	GGC	TCC	AAG	GTC	CTG	GCC	AAG	AAA	GAG	CTG							535
Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu							
			115					120					125								
GCC	TAT	GTC	CCA	ATT	ATC	GGC	TGG	ATG	TGG	TAC	TTC	ACC	GAG	ATG							580
Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met	Trp	Tyr	Phe	Thr	Glu	Met							
			130					135					140								
GTC	TTC	TGT	TCG	CGC	AAG	TGG	GAG	CAG	GAT	CGC	AAG	ACG	GTT	GCC							625
Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln	Asp	Arg	Lys	Thr	Val	Ala</							

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Figure 12

	10	20	30	40	50
LPAAT-γ1	MGLLAFLKTQ	FVLHLLVGfV	FVVSGLVINF	VQ-LCTLALW	PVSKQLYRRRL
LPAAT-γ2	-----	-----	-----	-----	-----
LPAAT-δ	MDLAGLLKSQ	FLCHLVFCYV	FIASGLIINT	IQ-LFTLLLW	PINKQLFRKI
	60	70	80	90	100
LPAAT-γ1	NCRLAYSLWS	QLVMLLEWWS	CTECTLFSTDQ	ATVERFGKEH	AVIILNHNFE
LPAAT-γ2	-----	---MLLEWWS	CTECTLFSTDQ	ATVERFGKEH	AVIILNHNFE
LPAAT-δ	NCRLSYCISS	QLVMLLEWWS	GTECTIFTDP	RAYLKYGKEN	AIVVLNHNKFE
	110	120	130	140	150
LPAAT-γ1	IDFLCGWTMC	ERFGVLGSSK	VLAKKELLYV	PLIGWTWYFL	EIVFCKRKWE
LPAAT-γ2	IDFLCGWTMC	ERFGVLGSSK	VLAKKELLYV	PLIGWTWYFL	EIVFCKRKWE
LPAAT-δ	IDFLCGWSHS	ERFGLLGGSK	VLAKKELAYV	PIIGWMWYFT	EMVFCRSRWE
	160	170	180	190	200
LPAAT-γ1	EDRDTVVEGL	RRLSDYPEYM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLPV
LPAAT-γ2	EDRDTVVEGL	RRLSDYPEYM	WFLLYCEGTR	FTETKHRVSM	EVAAAKGLPV
LPAAT-δ	QDRKTVATSL	QHLRDYPEKY	FFLIHCEGTR	FTEKKHEISM	QVARAKGLPR
	210	220	230	240	250
LPAAT-γ1	LKYHLLPRTK	GFTTAVKCLR	GTVAAYVDVT	LNF-RGNKNP	SLLGILYGKK
LPAAT-γ2	LKYHLLPRTK	GFTTAVKCLR	GTVAAYVDVT	LNF-RGNKNP	SLLGILYGKK
LPAAT-δ	LKHLLPRTK	GFAITVRSLR	NVSAVYDCT	LNF-RNNENP	LLGLVNGKK
	260	270	280	290	300
LPAAT-γ1	YEADMCVRRF	PLEDIPLDEK	EAAQWLHKLY	QEKDALQEIY	NQKGMFPGEQ
LPAAT-γ2	YEADMCVRRF	PLEDIPLDEK	EAAQWLHKLY	QEKDALQEIY	NQKGMFPGEQ
LPAAT-δ	YHADLYVRRI	PLEDIPEDDD	ECSAWLHKLY	QEKDAFQEEY	YRTGTFFPPTP
	310	320	330	340	350
LPAAT-γ1	FKPARRPWTl	LNFLSWATIL	LSPLFSFVLG	VFASGSPLLI	---LTFLGfV
LPAAT-γ2	FKPARRPWTl	LNFLSWATIL	LSPLFSFVLG	VFASGSPLLI	---LTFLGfV
LPAAT-δ	MVPPRRPWTl	VNWLFWASLV	LYPFFQFLVS	MIRSGSSLTL	---ASFILVF
	360	370	380		
LPAAT-γ1	GAASFGVRRl	IGVTEIEKGS	SYGNQEF--K	KKE*	
LPAAT-γ2	GAASFGVRRl	IGVTEIEKGS	SYGNQEF--K	KKE*	
LPAAT-δ	FVASVGVRWM	IGVTEIDKGS	AYGNSDSKQK	LND*	

Figure 13

